AMENDMENTS TO THE CLAIMS:

Pursuant to 37 C.F.R. § 1.121, the following listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-87. (Canceled)

88. (Currently Amended) An interferon β polypeptide variant exhibiting interferon β activity, comprising a variant sequence which differs from the wild-type human interferon β sequence SEQ ID NO:2 in no more than 15 amino acid residues, the variant sequence comprising (a) at least one introduced N-glycosylation site comprising two amino acid substitutions relative to SEQ ID NO:2 selected from the group consisting of Q49N+Q51T/S and F111N+R113T/S, and (b) an amino acid substitution at position –1 relative to at least one of the introduced N-glycosylation site(s).

89. (Currently Amended) The variant according to claim 88, further comprising ~~wherein~~ at least one ~~of the N-glycosylation site(s) is a~~ naturally occurring N-glycosylation site.

90-91. (Canceled)

92. (Currently Amended) The variant according to claim 88 ~~90~~, wherein the variant comprises at least two introduced N-glycosylation sites.

93. (Canceled)

94. (Previously Presented) The variant according to claim 88, further comprising at least one non-polypeptide moiety covalently attached to the variant.

95. (Previously Presented) The variant according to claim 94, comprising at least one sugar moiety and at least one polymer molecule.

96. (Previously Presented) The variant according to claim 95, wherein at least one of the polymer molecule(s) is covalently attached to a lysine residue of the variant.

97. (Previously Presented) The variant according to claim 95, wherein at least one of the polymer molecule(s) is covalently attached to the N-terminus of the variant.

98. (Previously Presented) The variant according to claim 95, wherein the polymer molecule comprises a linear polyethylene glycol or a branched polyethylene glycol.

99. (Previously Presented) A composition comprising the variant of claim 88 or 94 and a pharmaceutically acceptable diluent, carrier, or excipient.

100-108. (Withdrawn)

109. (New) The variant according to claim 88, wherein the at least one introduced N-glycosylation site comprises substitutions Q49N+Q51T/S relative to SEQ ID NO:2.

110. (New) The variant according to claim 109, wherein the amino acid substitution at position -1 relative to the at least one introduced N-glycosylation site comprising substitutions Q49N+Q51T/S is selected from the group consisting of Q48F, Q48V, Q48W, and Q48Y.

111. (New) The variant according to claim 88, wherein the at least one introduced N-glycosylation site comprises substitutions F111N+R113T relative to SEQ ID NO:2.

112. (New) The variant according to claim 111, wherein the amino acid substitution at position -1 relative to the at least one introduced N-glycosylation site comprising substitutions F111N+R113T/S is selected from the group consisting of D110F, D110V, D110W, and D110Y.

113. (New) The variant according to claim 112, wherein the amino acid substitution at position -1 relative to the at least one introduced N-glycosylation site comprising substitutions F111N+R113T/S is D110F.

114. (New) The variant according to claim 92, wherein the at least two introduced N-glycosylation sites comprise substitutions Q49N+Q51T and F111N+R113T.

115. (New) The variant according to claim 114, wherein the amino acid substitution at position -1 relative to the introduced N-glycosylation site comprising substitutions Q49N+Q51T is selected from the group consisting of Q48F, Q48V, Q48W, and Q48Y and the amino acid substitution at position -1 relative to the introduced N-glycosylation site comprising substitutions F111N+R113T is selected from the group consisting of D110F, D110V, D110W, and D110Y.

116. (New) The variant according to claim 88, further comprising the amino acid substitution C17S.

117. (New) The variant according to claim 115, further comprising the amino acid substitution C17S.